

GenCore version 6.2  
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OW protein - protein search, using sw model

Run on: February 1, 2007, 12:18:59 ; Search time 218 Seconds

(without alignments)  
78.563 Million cell updates/sec

Title: US-10-530-125A-15

Perfect score: 180

Sequence: 1 HSEGTFTSDVSSYLEGQAKEFTIAVLVKGKKKKR 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 48933398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_200701.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

10: Geneseqp2006s.\*

11: Geneseqp2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	35	8 ADO44524	Ado44524 Human GLP
2	177	98.3	37	8 ADO44525	Ado44525 Human GLP
3	177	98.3	40	8 ADO44526	Ado44526 Human GLP
4	171	95.0	35	8 ADO44532	Ado44532 Human GLP
5	171	95.0	36	2 ADI24914	Adi24914 GLP-1 (?)
6	170	94.4	36	4 AAB69960	Aab69960 Gly8-GLP-

7	170	94.4	36	4 AAB69973	Aab69973 Gly8, Lys
8	170	94.4	36	4 AAB69972	Aab69972 Gly8-GLP-
9	170	94.4	36	4 AAB69974	Aab69974 Gly8, Lys
10	170	94.4	38	4 AAB69961	Aab69961 Gly8, Lys
11	170	94.4	38	4 AAB69977	Aab69977 Gly8-GLP-
12	170	94.4	40	4 AAB69978	Aab69978 Gly8-GLP-
13	170	94.4	42	4 AAB69975	Aab69975 (Lys)6-Gl
14	167	92.8	33	8 ADO44523	Ado44523 Human GLP
15	165	91.7	35	8 ADO44518	Ado44518 Human GLP
16	165	91.7	36	8 ADO44519	Ado44519 Human GLP
17	165	91.7	38	8 ADO44520	Ado44520 Human GLP
18	162	90.0	32	8 ADO44522	Ado44522 Human GLP
19	162	90.0	32	8 ADO44527	Ado44527 Human GLP
20	160	88.9	34	8 ADO44533	Ado44533 Human GLP
21	160	88.9	34	8 ADO44517	Ado44517 Human GLP
22	158	87.8	33	8 ADO44516	Ado44516 Human GLP
23	158	87.8	34	8 ADO44534	Ado44534 Human GLP
24	157	87.2	31	8 ADO44521	Ado44521 Human GLP
25	156	86.7	32	8 ADO44515	Ado44515 Human GLP
26	156	86.7	36	8 ADO44531	Ado44531 Human GLP
27	154	85.6	31	4 AAB48813	Aab48813 Insulinot
28	154	85.6	31	4 AAB48814	Aab48814 Insulinot
29	154	85.6	31	4 AAB48806	Aab48806 Insulinot
30	154	85.6	31	4 AAB91196	Aab91196 Pancreati
31	154	85.6	31	4 AAB83290	Aab83290 GLP-1 pep
32	154	85.6	31	9 AED86981	Aed86981 GLP-1 ana
33	154	85.6	31	9 AED86959	Aed86959 GLP-1 ana
34	154	85.6	31	9 AED86967	Aed86967 GLP-1 ana
35	154	85.6	31	9 AED86968	Aed86968 GLP-1 ana
36	154	85.6	31	9 AED86982	Aed86982 GLP-1 ana
37	154	85.6	31	10 AEG41157	Aeg41157 Insulinot
38	154	85.6	31	10 AEG77116	Aeg77116 Human glu
39	154	85.6	31	10 AEI38972	AEi38972 CJC-1131.
40	154	85.6	31	10 AEI67293	AEi67293 Exendin-4
41	154	85.6	31	10 AEJ64360	AEj64360 Oligosacc
42	154	85.6	31	10 AEL18628	Ael18628 Partner p
43	154	85.6	32	2 AAY42949	Aay42949 Xaa8.Glu3
44	154	85.6	32	2 AAY42948	Aay42948 Xaa8.Glu3
45	154	85.6	37	4 AAB48805	Aab48805 Insulinot

#### ALIGNMENTS

RESULT 1

ADO44524

ID ADO44524 standard; peptide; 35 AA.

XX

AC ADO44524;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human GLP-1 peptide derivative 8S-des36R-GLP1+5KR.

XX

KW GLP-1; glucagon-like peptide 1; dipeptidylpeptidase IV; trypsin;

XX antidiabetic; anorectic; insulin secretion.

OS Homo sapiens.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site 35  
 FT /note= "C-terminal amide"  
 XX  
 FN WO2004037859-A1.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-JP013020.  
 XX  
 PR 11-OCT-2002; 2002JP-00299283.  
 XX  
 PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.  
 XX  
 PI Hayashi Y, Makino M, Kouzaki T, Takeda M, Jomori T;  
 XX  
 DR WPI; 2004-357426/33.  
 XX  
 PT New glucagon-like peptide 1 derivatives comprising an added C-terminal  
 PT peptide, with improved transmembrane absorbability used for the treatment  
 PT of diabetes.  
 XX  
 PS Example 1; SEQ ID NO 15; 48pp; Japanese.  
 XX  
 CC The invention relates to peptides consisting of a sequence derived from  
 CC glucagon-like peptide 1 (GLP-1) residues 7-35 by addition, deletion  
 CC and/or substitution of one or more amino acid residues. The GLP-1 derived  
 CC peptides have an added sequence at the C-terminal of formula Waa-(Xaa)n-  
 CC Yaa, where Waa is arginine or lysine; Xaa is arginine or lysine; Yaa is  
 CC arginine, arginine amide, lysine, lysine amide or homoserine; and n is 0-  
 CC 14. The GLP-1 peptide derivatives have tolerance to dipeptidylpeptidase  
 CC IV and to trypsin due to the nature of the substitution. The peptides can  
 CC be synthesised by standard solid-state peptide synthesis methods. The  
 CC peptides can be used in the treatment of diabetes (insulin-dependent or  
 CC insulin non-dependent), obesity and excessive appetite. Sequences  
 CC ADO44512-ADO44534 represent examples of GLP-1 peptide derivatives.  
 XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 180; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 HSEGTFTSDVSSYLEGQAAKEFIWLKGGKKKKR 35  
 |||||  
 DB 1 HSEGTFTSDVSSYLEGQAAKEFIWLKGGKKKKR 35  
 |||||  
 RESULT 2  
 ADO44525  
 ID ADO44525 standard; peptide; 37 AA.  
 XX  
 AC ADO44525;  
 XX

DT 29-JUL-2004 (first entry)  
 XX Human GLP-1 peptide derivative 8S-des36R-GLP1+7KR.  
 XX  
 KW GLP-1; glucagon-like peptide 1; dipeptidylpeptidase IV; trypsin;  
 KW antidiabetic; anorectic; insulin secretion.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 37  
 FT /note= "C-terminal amide"  
 XX  
 FN WO2004037859-A1.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-JP013020.  
 XX  
 PR 11-OCT-2002; 2002JP-00299283.  
 XX  
 PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.  
 XX  
 PI Hayashi Y, Makino M, Kouzaki T, Takeda M, Jomori T;  
 XX  
 DR WPI; 2004-357426/33.  
 XX  
 PT New glucagon-like peptide 1 derivatives comprising an added C-terminal  
 PT peptide, with improved transmembrane absorbability used for the treatment  
 PT of diabetes.  
 XX  
 PS Example 1; SEQ ID NO 16; 48pp; Japanese.  
 XX  
 CC The invention relates to peptides consisting of a sequence derived from  
 CC glucagon-like peptide 1 (GLP-1) residues 7-35 by addition, deletion  
 CC and/or substitution of one or more amino acid residues. The GLP-1 derived  
 CC peptides have an added sequence at the C-terminal of formula Waa-(Xaa)n-  
 CC Yaa, where Waa is arginine or lysine; Xaa is arginine or lysine; Yaa is  
 CC arginine, arginine amide, lysine, lysine amide or homoserine; and n is 0-  
 CC 14. The GLP-1 peptide derivatives have tolerance to dipeptidylpeptidase  
 CC IV and to trypsin due to the nature of the substitution. The peptides can  
 CC be synthesised by standard solid-state peptide synthesis methods. The  
 CC peptides can be used in the treatment of diabetes (insulin-dependent or  
 CC insulin non-dependent), obesity and excessive appetite. Sequences  
 CC ADO44512-ADO44534 represent examples of GLP-1 peptide derivatives.  
 XX  
 SQ Sequence 37 AA;  
 Query Match 98.3%; Score 177; DB 8; Length 37;  
 Best Local Similarity 97.1%; Pred. No. 3.3e-17;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 HSEGTFTSDVSSYLEGQAAKEFIWLKGGKKKKR 35  
 |||||  
 DB 1 HSEGTFTSDVSSYLEGQAAKEFIWLKGGKKKKR 35  
 |||||

GenCore version 6.2  
Copyright (c) 1993 - 2007 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 1, 2007, 12:21:34 ; Search time 346 Seconds  
(without alignments)  
108.452 Million cell updates/sec

Title: US-10-530-125A-15  
Perfect score: 180  
Sequence: 1 HSEGTFTSDVSSYLEGQAAKEFIAMLVKGGKKKKR 35  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 3281787 seqs, 1072124677 residues  
Total number of hits satisfying chosen parameters: 3281787  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot\_8.4.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
1	151	83.9	45 2 Q6PPF4 CAPHI
2	151	83.9	176 1 GLUC_SHEEP
3	151	83.9	180 1 GLUC_BOVIN
4	151	83.9	180 1 GLUC_CANFA
5	151	83.9	180 1 GLUC_CAVPO
6	151	83.9	180 1 GLUC_HUMAN
7	151	83.9	180 1 GLUC_MESAU
8	151	83.9	180 1 GLUC_MOUSE
9	151	83.9	180 1 GLUC_OCTDE
10	151	83.9	180 1 GLUC_PIG
11	151	83.9	180 1 GLUC_RAT
12	151	83.9	180 2 Q53TP6 HUMAN
13	140	77.8	151 2 Q3HLJ2_MELGA
14	140	77.8	151 2 Q3HWX1_CHICK
15	139	77.2	124 2 Q6RYB1_9SAUR

16	139	77.2	206 1 GLUC_CHICK	P68259 g glucagon
17	139	77.2	206 2 Q3HLJ2_MELGA	Q3hlj2 meleagris g
18	139	77.2	206 2 Q3HWX1_CHICK	Q3hwx1 gallus gall
19	137	76.1	80 2 Q6IUP8_PHOSU	Q6iup8 phodopus su
20	133	73.9	145 2 Q6RYB5_NEOFS	Q6ryb5 neoceratodu
21	133	73.9	204 1 GLUC_HESLU	O12956 h glucagon
22	132	73.3	266 1 GLUC1_XENLA	O42143 xenopus lae
23	131	72.8	220 2 Q8UW19_NEOB	Q8uw19 hophobatrac
24	130	72.2	153 2 Q6RYB6_PRODO	Q6ryb6 protopterius
25	127	70.6	103 1 GLUC_RANCA	P15438 rana catesb
26	127	70.6	266 2 Q6DIZ4_XENTR	Q6diz4 xenopus tro
27	125	69.4	149 2 Q6RYB2_BUFMA	Q6ryb2 bufo marinu
28	125	69.4	219 1 GLUC2_XENLA	O42144 xenopus lae
29	125	69.4	219 2 Q5D082_XENLA	Q5d082 xenopus lae
30	120	66.7	30 1 GLUC1_ANGAN	P63294 anguilla an
31	120	66.7	30 1 GLUC1_ANGRO	P63295 anguilla ro
32	118	65.6	120 2 Q6RYB7_ICTPU	Q6ryb7 ictalurus p
33	118	65.6	121 2 Q5PR39_BRARE	Q5pr39 brachydanio
34	118	65.6	122 2 Q6RYB8_ICTPU	Q6ryb8 ictalurus p
35	117	65.0	71 1 GLUC1_ICTPU	Q6ryb9 ictalurus p
36	117	65.0	71 1 GLUC1_PIAPE	P04093 ictalurus p
37	117	65.0	71 1 GLUC1_PIAPE	P81880 piaractus m
38	117	65.0	78 1 GLUC1_LEFSP	P09566 lepisosteus
39	117	65.0	122 1 GLUC2_LOPAM	P04092 lophius ame
40	117	65.0	123 2 Q6RYA9_9PERC	Q6rya9 sebastes ca
41	117	65.0	860 2 Q4RQJ4_TETNG	Q4rqj4 tetraodon n
42	116	64.4	66 2 Q788W6_ONCTS	Q788w6 oncorhynch
43	116	64.4	72 2 Q91409_ONCTS	Q91409 oncorhynch
44	116	64.4	178 1 GLUC1_ONCMY	Q91371 oncorhynch
45	113	62.8	121 1 GLUC1_ORCAU	P79695 carassius a

ALIGNMENTS

RESULT 1  
Q6PPF4 CAPHI  
ID Q6PPF4 CAPHI PRELIMINARY; PRT; 45 AA.  
AC Q6PPF4;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE Glucagon (Fragment).  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Caprinae; Capra.  
OX NCBI\_TaxID=9925;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Ballester M., Castello A., Ibanez E., Sanchez A., Folch J.M.;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC EMBL; AY588290; AA00451.1; -; Genomic\_DNA.  
DR

DR GO: GO:000576; C:extracellular region; IEA.  
DR GO: GO:0005179; F:hormone activity; IEA.  
DR InterPro: IPR000532; Glucagon.  
DR Pfam: PF00123; Hormone.2; 1.  
DR PRINTS: PR00275; GLUCAGON.  
DR SMART: SM00070; GLUCA; 1.  
DR NON\_TER 1 1  
FT NON\_TER 45 45  
SQ SEQUENCE 45 AA; 5179 MW; B538A926E9447F80 CRC64;

Query Match 83.9%; Score 151; DB 2; Length 45;  
Best Local Similarity 84.8%; Pred. No. 2.1e-12;  
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSEGTFTSDVSSYLEGQAAKEFIAWLKRGKKK 33  
|:|||||:|||||:|||||:|||||:|:  
Db 13 HAETFTSDVSSYLEGQAAKEFIAWLKRGRR 45

RESULT 2  
ID GLUC\_SHEEP STANDARD; PRT; 176 AA.  
AC QPMJ25;

DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-2002, sequence version 1.  
DT 27-JUN-2006, entry version 18.  
DE Glucagon precursor [Contains: Glucagon; Glucagon-related polypeptide  
DE (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1  
DE (GLP-1); Glucagon-like peptide 1 (7-37) (GLP-1(7-37)); Glucagon-like  
DE peptide 1 (7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]  
DE (Fragment).  
DE Name=GGC;  
GN Ovis aries (Sheep).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Pancreas;  
RA Limesand S.W., Hay W.W. Jr.;  
RT "Characterization of the endocrine pancreas in an ovine placental  
RT insufficiency IUGR fetus."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Glucagon plays a key role in glucose metabolism and  
CC homeostasis. Regulates blood glucose by increasing gluconeogenesis  
CC and decreasing glycolysis. A counterregulatory hormone of insulin,  
CC raises plasma glucose levels in response to insulin-induced  
CC hypoglycemia (By similarity).  
CC -!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent  
CC insulin release. Play important roles on gastric motility and the  
CC suppression of plasma glucagon levels. May be involved in the  
CC suppression of satiety and stimulation of glucose disposal in  
CC peripheral tissues, independent of the actions of insulin. Have  
CC growth-promoting activities on intestinal epithelium. May also  
CC regulate the hypothalamic pituitary axis (HPA) via effects on LH,  
CC TSH, CRH, oxytocin, and vasopressin (By similarity).

CC -!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates  
CC villus height in the small intestine, concomitant with increased  
CC crypt cell proliferation and decreased enterocyte apoptosis. The  
CC gastrointestinal tract, from the stomach to the colon is the  
CC principal target for GLP-2 action. Plays a key role in nutrient  
CC homeostasis, enhancing nutrient assimilation through enhanced  
CC gastrointestinal function, as well as increasing nutrient  
CC disposal. Stimulates intestinal glucose transport and decreases  
CC mucosal permeability (By similarity).  
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By  
CC similarity).  
CC -!- FUNCTION: Glucagon may modulate gastric acid secretion and  
CC gastro-pyloro-duodenal activity.  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the  
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glicentin  
CC are secreted from enteroendocrine cells throughout the  
CC gastrointestinal tract. GLP1 and GLP2 are also secreted in  
CC selected neurons in the brain.  
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and  
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and  
CC GLP-2 are induced in response to nutrient ingestion (By  
CC similarity).  
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-  
CC specific manner in pancreatic A cells and intestinal L cells. In  
CC pancreatic A cells, the major bioactive hormone is glucagon  
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1  
CC liberates GLP-1, GLP-2, glicentin and oxyntomodulin. GLP-1 is  
CC further N-terminally truncated by posttranslational processing in  
CC the intestinal L cells resulting in GLP-1(7-37) GLP-1-(7-36)amide.  
CC The C-terminal amidation is neither important for the metabolism  
CC of GLP-1 nor for its effects on the endocrine pancreas (By  
CC similarity).  
CC -!- MISCELLANEOUS: GLP-2 does not have cleavage on a pair of basic  
CC residues at C-terminus as in other mammals.  
CC -!- SIMILARITY: Belongs to the glucagon family.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC ENBL: AF529185; AAM94409.1; -, mRNA.  
CC InterPro: IPR000532; Glucagon.  
CC Pfam: PF00123; Hormone.2; 3.  
CC PRINTS: PR00275; GLUCAGON.  
CC SMART: SM00070; GLUCA; 3.  
CC PROSITE: PS00260; GLUCAGON; 4.  
CC Anidation; Cleavage on pair of basic residues; Hormone; Signal.  
CC SIGNAL 1 20  
CC PEPTIDE 21 89 Glicentin (By similarity).  
CC /FTId-PRO\_0000011313.  
CC PEPTIDE 21 50 Glicentin-related polypeptide (By  
CC similarity).  
CC /FTId-PRO\_0000011314.  
CC PEPTIDE 53 89 Oxyntomodulin (By similarity).  
CC /FTId-PRO\_0000011315.  
CC PEPTIDE 53 81 Glucagon.  
CC /FTId-PRO\_0000011316..

OM protein - protein search, using sw model

Run on: February 1, 2007, 12:24:23 ; Search time 39 Seconds  
(without alignments)  
86.348 Million cell updates/sec

Title: US-10-530-125A-15  
Perfect score: 180  
Sequence: 1 HSEGTFTSDVSSYLEGQAKEFIAMLVKGGKKKKR 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	83.9	180	1 GCBO	glucagon precursor
2	151	83.9	180	1 GCHY	glucagon precursor
3	151	83.9	180	1 GCGP	glucagon precursor
4	151	83.9	180	1 GCHU	glucagon precursor
5	151	83.9	180	1 GCRT	glucagon precursor
6	151	83.9	180	1 GCRTDU	glucagon precursor
7	151	83.9	180	2 A57294	glucagon precursor
8	149	82.8	158	1 GCPG	glucagon precursor
9	140	77.8	151	1 GCCH	proglucagon - chic
10	139	77.2	206	2 I51301	glucagon precursor
11	127	70.6	101	1 GCFCB	glucagon-like pept
12	120	66.7	30	2 C61125	glucagon-like pept
13	120	66.7	30	2 B61125	glucagon-like pept

14	118	65.6	63	1 GCIDC	glucagon precursor
15	117	65.0	72	1 GCGXA	glucagon precursor
16	117	65.0	122	1 GCAF2	glucagon 2 precurs
17	116	64.4	66	2 I51093	glucagon - chinook
18	116	64.4	178	2 I51058	glucagon I precurs
19	113	62.8	178	2 I51057	glucagon II precurs
20	108	60.0	30	2 S44473	glucagon-like pept
21	107	59.4	60	1 GCNC	glucagon precursor
22	103	57.2	69	1 GCDG69	glucagon-69 - dog
23	103	57.2	87	1 GCRIS	glucagon precursor
24	102	56.7	31	2 S44472	glucagon G2 - Nort
25	101	56.1	124	1 GCAF	glucagon 1 precurs
26	100	55.6	29	2 S07211	glucagon - marbled
27	100	55.6	31	2 S44471	glucagon G1 - Nort
28	98	54.4	29	1 GCDF	glucagon - smaller
29	96	53.3	29	1 GCEN	glucagon - elephant
30	93	51.7	29	1 GCOFV	glucagon - North A
31	93	51.7	29	2 A91740	glucagon - turkey
32	93	51.7	29	2 C39258	glucagon - common
33	93	51.7	29	2 A91742	glucagon - Arabian
34	93	51.7	29	2 A91741	glucagon - rabbit
35	91	50.6	29	1 A61583	glucagon - ostrich
36	91	50.6	29	1 GCDK	glucagon - duck
37	91	50.6	29	1 GCTTS	glucagon - slider
38	91	50.6	29	2 C60840	glucagon I - Europ
39	89	50.0	29	1 GCCB	glucagon - Chinch
40	89	49.4	29	1 GCFL	glucagon - Europea
41	89	49.4	29	2 A61135	glucagon - bigeye
42	88	48.9	39	1 HMGH32	extendin-3 - Mexica
43	87	48.3	39	1 HMGH4G	extendin-4 - Gila m
44	86	47.8	29	2 S39018	glucagon - bowfin
45	85	47.2	36	1 GCFI	glucagon-36 - spot

#### ALIGNMENTS

##### RESULT 1

GCBO

glucagon precursor - bovine  
N;Contains: glucagon-related peptide; glucagon; glucagon-like peptide 1;  
glucagon-like peptide 2  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 20-Mar-1998  
C;Accession: A93970; A92081; A01538  
R;Lopez, L.C.; Frazier, M.L.; Su, C.J.; Kumar, A.; Saunders, G.F.  
Proc. Natl. Acad. Sci. U.S.A. 80, 5485-5489, 1983  
A;Title: Mammalian pancreatic preproglucagon contains three glucagon-related  
peptides.  
A;Reference number: A93970; MUID:83299996; PMID:6577439  
A;Accession: A93970  
A;Molecule type: mRNA  
A;Residues: 1-180 <LOP>  
A;Cross-references: UNIPARC:UPI0001734FF; EMBL:K00107  
R;Brumer, W.W.; Boucher, M.E.; Koffenberger Jr., J.E.  
J. Biol. Chem. 246, 2822-2827, 1971  
A;Title: Amino acid sequence of bovine glucagon.

A;Reference number: A92081; MUID:71166445; PMID:5102927

A;Accession: A92081

A;Molecule type: protein

A;Residues: 53-81 <BRO>

A;Cross-references: UNIPARC:UPI000002C586

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancreas

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-180/Product: proglucagon #status predicted <PGC>

F;21-50/Region: glicentin-related peptide #status predicted

F;53-81/Product: glucagon #status experimental <GCN>

F;98-127/Product: glucagon-like peptide 1 #status experimental <GL1>

F;146-180/Product: glucagon-like peptide 2 #status predicted <GL2>

F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glycine) #status predicted

Query Match 83.9%; Score 151; DB 1; Length 180;

Best Local Similarity 84.8%; Pred. No. 5e-13;

Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSEGTFTSDVSSYLEGQAQKEFIANLVKGRKK 33

DB 98 HAEGTFTSDVSSYLEGQAQKEFIANLVKGRGR 130

RESULT 2

GCGY

Glucagon precursor - golden hamster

N;Contains: glicentin-related peptide; glucagon; glucagon-like peptide 1;

glucagon-like peptide 2

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 20-Mar-1998

C;Accession: A01539

R;Bell, G.I.; Santerre, R.F.; Mullenbach, G.T.

Nature 302, 716-718, 1983

A;Title: Hamster preproglucagon contains the sequence of glucagon and two related peptides.

A;Reference number: A01539; MUID:83167563; PMID:6835407

A;Accession: A01539

A;Molecule type: mRNA

A;Residues: 1-180 <BEL>

A;Cross-references: UNIPARC:UPI00001734FE; EMBL:J00059

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancreas

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-180/Product: proglucagon #status predicted <PGC>

F;21-50/Region: glicentin-related peptide #status predicted

F;53-81/Product: glucagon #status predicted <GCN>

F;98-127/Product: glucagon-like peptide 1 #status predicted <GL1>

F;146-180/Product: glucagon-like peptide 2 #status predicted <GL2>

F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glycine) #status predicted

Query Match 83.9%; Score 151; DB 1; Length 180;

Best Local Similarity 84.8%; Pred. No. 5e-13;

Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSEGTFTSDVSSYLEGQAQKEFIANLVKGRKK 33

DB 98 HAEGTFTSDVSSYLEGQAQKEFIANLVKGRGR 130

RESULT 3

GCGP

glucagon precursor - guinea pig

N;Alternate names: oxyntomodulin

N;Contains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin);

glucagon-like peptide 1; glucagon-like peptide 2

C;Species: Cavia porcellus (guinea pig)

C;Date: 30-Sep-1987 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C;Accession: A24856; A23849; A60323

R;Seino, S.; Welsh, M.; Bell, G.I.; Chan, S.J.; Steiner, D.F.

FEBS Lett. 203, 25-30, 1986

A;Title: Mutations in the guinea pig preproglucagon gene are restricted to a specific portion of the prohormone sequence.

A;Reference number: A24856; MUID:86248118; PMID:3755107

A;Accession: A24856

A;Molecule type: mRNA

A;Residues: 1-180 <SEI>

A;Cross-references: UNIPROT:POS110; UNIPARC:UPI000012B82C; DBPJ:D00014;

CB:N00014; NID:9220288; PIDN:BAA00010.1; PID:9220289

R;Huang, C.G.; Eng, J.; Pan, Y.C.E.; Hulmes, J.D.; Yalow, R.S.

Diabetes 35, 508-512, 1986

A;Title: Guinea pig glucagon differs from other mammalian glucagons.

A;Reference number: A23849; MUID:86165412; PMID:3956884

A;Accession: A23849

A;Molecule type: protein

A;Residues: 53-81 <HUA>

A;Cross-references: UNIPARC:UPI00001734FD

R;Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.

Regul. Pept. 11, 309-320, 1985

A;Title: Primary structure of glucagon and a partial sequence of oxyntomodulin (glucagon-37) from the guinea pig.

A;Reference number: A60323; MUID:86017849; PMID:4048553

A;Accession: A60323

A;Molecule type: protein

A;Residues: 53-81 <CON>

A;Cross-references: UNIPARC:UPI00001734FD

A;Note: glucagon-37 was not completely sequenced

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancreas

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-180/Product: proglucagon #status predicted <PGC>

F;21-50/Region: glicentin-related peptide #status predicted

F;53-81/Product: glucagon #status experimental <GCN>

F;98-127/Product: glucagon-like peptide 1 #status predicted <GL1>

F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>

F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glycine) #status predicted